

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Lin, Lih-Ling
Graham, James

(ii) TITLE OF INVENTION: NOVEL INTERLEUKIN-1 RECEPTOR
INTRACELLULAR LIGAND PROTEINS AND INHIBITORS OF LIGAND
BINDING

(iii) NUMBER OF SEQUENCES: 7

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: LEGAL AFFAIRS, GENETICS INSTITUTE, INC.
(B) STREET: 87 CambridgePark Drive
(C) CITY: Cambridge
(D) STATE: MA
(E) COUNTRY: USA
(F) ZIP: 02140

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Brown, Scott A.
(B) REGISTRATION NUMBER: 32,724
(C) REFERENCE/DOCKET NUMBER: GI5258

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (617) 498-8224
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1571 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 2..529

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

G ATC CCC AGG GTG GAC CTC CGG GTG TGG CAG GAC TGC TGT GAA GAC
Ile Pro Arg Val Asp Leu Arg Val Trp Gln Asp Cys Cys Glu Asp
1 5 10 15

46

E05 E06 E07 E08 E09 E10 E11 E12 E13 E14

TGT AGG ACC AGG GGG CAG TTC AAT GCC TTT TCC TAT CAT TTC CGA GGC Cys Arg Thr Arg Gly Gln Phe Asn Ala Phe Ser Tyr His Phe Arg Gly 20 25 30	94
AGA CGG TCT CTT GAG TTC AGC TAC CAG GAG GAC AAG CCG ACC AAG AAA Arg Arg Ser Leu Glu Phe Ser Tyr Gln Glu Asp Lys Pro Thr Lys Lys 35 40 45	142
ACA AGA CCA CGG AAA ATA CCC AGT GTT GGG AGA CAG GGG GAA CAT CTC Thr Arg Pro Arg Lys Ile Pro Ser Val Gly Arg Gln Gly Glu His Leu 50 55 60	190
AGC AAC AGC ACC TCA GCC TTC AGC ACA CGC TCA GAT GCA TCT GGG ACA Ser Asn Ser Thr Ser Ala Phe Ser Thr Arg Ser Asp Ala Ser Gly Thr 65 70 75	238
AAT GAC TTC AGA GAG TTT GTT CTG GAA ATG CAG AAG ACC ATC ACA GAC Asn Asp Phe Arg Glu Phe Val Leu Glu Met Gln Lys Thr Ile Thr Asp 80 85 90 95	286
CTC AGA ACA CAG ATA AAG AAA CTT GAA TCA CGG CTC AGT ACC ACA GAG Leu Arg Thr Gln Ile Lys Lys Leu Glu Ser Arg Leu Ser Thr Thr Glu 100 105 110	334
TGC GTG GAT GCC GGG GGC GAA TCT CAC GCC AAC AAC ACC AAG TGG AAA Cys Val Asp Ala Gly Gly Glu Ser His Ala Asn Asn Thr Lys Trp Lys 115 120 125	382
AAA GAT GCA TGC ACC ATT TGT GAA TGC AAA GAC GGG CAG GTC ACC TGC Lys Asp Ala Cys Thr Ile Cys Glu Cys Lys Asp Gly Gln Val Thr Cys 130 135 140	430
TTC GTG GAA GCT TGC CCC CCT GCC ACC TGT GCT GTC CCC GTG AAC ATC Phe Val Glu Ala Cys Pro Pro Ala Thr Cys Ala Val Pro Val Asn Ile 145 150 155	478
CCA GGG GCC TGC TGT CCA GTC TGC TTA CAG AAG AGG GCG GAG GAA AAG Pro Gly Ala Cys Cys Pro Val Cys Leu Gln Lys Arg Ala Glu Glu Lys 160 165 170 175	526
CCC TAGGCTCCTG GGAGGCTCCT CAGAGTTGT CTGCTGTGCC ATCGTGAGAT Pro	579
CGGGTGGCCG ATGGCAGGGA GCTGCGGACT GCAGACCAGG AAACACCCAG AACTCGTGAC	639
ATTTCATGAC AACGTCCAGC TGGTGCTGTT ACAGAAGGCA GTGCAGGAGG CTTCCAACCA	699
GAGCATCTGC GGAGAAGGAG GCACAGCAGG TGCTGAAGG GAAGCAGGCA GGAGTCCTAG	759
CTTCACGTTA GACTTCTCAG GTTTTTATTT AATTCTTTA AAATGAAAAAA TTGGTGCTAC	819
TATTAATTG CACAGTTGAA TCATTTAGGC GCCTAAATTG ATTTTGCTCTC CCAACACCAT	879
TTCTTTTAA ATAAAGCAGG ATACCTCTAT ATGTCAGCCT TGCCTGTTC AGATGCCAGG	939
AGCCGGCAGA CCTGTCACCC GCAGGTGGGG TGAGTCTCGG AGCTGCCAGA GGGGCTCAC	999
GAAATCGGGG TTCCATCACA AGCTATGTTT AAAAGAAAAA TTGGTGTTG CCAAACGGAA	1059
CAGAACCTT GATGAGAGCG TTCACAGGGA CACTGTCTGG GGGTGCAGTG CAAGCCCCG	1119
GCCTCTTCCC TGGGAACCTC TGAACTCCTC CTTCTCTGG GCTCTCTGTA ACATTTCAC	1179
ACACGTCAGC ATCTAATCCC AAGACAAACA TTCCCGCTGC TCGAAGCAGC TGTATAGCCT	1239
GTGACTCTCC GTGTGTCAGC TCCTTCCACA CCTGATTAGA ACATTCTAA GCCACATTAA	1299

GAAACAGGTT TGCTTTCAGC TGTCACTTGC ACACATACTG CCTAGTTGTG AACCAAATGT	1359
GAAAAAACCT CCTTCATCCC ATTGTGTATC TGATACCTGC CGAGGGCAA GGGTGTGTGT	1419
TGACAACGCC GCTCCCAGCC GGCCCTGGTT GCGTCCACGT CCTGAACAAG AGCCGCTTCC	1479
GGATGGCTCT TCCCAAGGGA GGAGGAGCTC AAGTGTGGG AACTGTCTAA CTTCAGGTTG	1539
TGTGAGTGCG TTAAAAAAAAA AAAAAAAAAA AA	1571

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 176 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Ile Pro Arg Val Asp Leu Arg Val Trp Gln Asp Cys Cys Glu Asp Cys	
1 5 10 15	
Arg Thr Arg Gly Gln Phe Asn Ala Phe Ser Tyr His Phe Arg Gly Arg	
20 25 30	
Arg Ser Leu Glu Phe Ser Tyr Gln Glu Asp Lys Pro Thr Lys Lys Thr	
35 40 45	
Arg Pro Arg Lys Ile Pro Ser Val Gly Arg Gln Gly Glu His Leu Ser	
50 55 60	
Asn Ser Thr Ser Ala Phe Ser Thr Arg Ser Asp Ala Ser Gly Thr Asn	
65 70 75 80	
Asp Phe Arg Glu Phe Val Leu Glu Met Gln Lys Thr Ile Thr Asp Leu	
85 90 95	
Arg Thr Gln Ile Lys Lys Leu Glu Ser Arg Leu Ser Thr Thr Glu Cys	
100 105 110	
Val Asp Ala Gly Gly Glu Ser His Ala Asn Asn Thr Lys Trp Lys Lys	
115 120 125	
Asp Ala Cys Thr Ile Cys Glu Cys Lys Asp Gly Gln Val Thr Cys Phe	
130 135 140	
Val Glu Ala Cys Pro Pro Ala Thr Cys Ala Val Pro Val Asn Ile Pro	
145 150 155 160	
Gly Ala Cys Cys Pro Val Cys Leu Gln Lys Arg Ala Glu Glu Lys Pro	
165 170 175	

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1088 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 2..961

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

G AAA AAA GGA GGT AAA ACA GAA CAG GAT GGC TAT CAG AAA CCC ACC Lys Lys Gly Gly Lys Thr Glu Gln Asp Gly Tyr Gln Lys Pro Thr 1 5 10 15	46
AAC AAA CAC TTC ACG CAG AGT CCC AAG AAG TCA GTG GCC GAC CTG CTG Asn Lys His Phe Thr Gln Ser Pro Lys Lys Ser Val Ala Asp Leu Leu 20 25 30	94
GGG TCC TTT GAA GGC AAA CGA AGA CTC CTT CTG ATC ACT GCT CCC AAG Gly Ser Phe Gly Lys Arg Arg Leu Leu Ile Thr Ala Pro Lys 35 40 45	142
GCT GAG AAC AAT ATG TAT GTG CAA CAA CGT GAT GAA TAT CTG GAA AGT Ala Glu Asn Asn Met Tyr Val Gln Gln Arg Asp Glu Tyr Leu Glu Ser 50 55 60	190
TTC TGC AAG ATG GCT ACC AGG AAA ATC TCT GTG ATC ACC ATC TTC GGC Phe Cys Lys Met Ala Thr Arg Lys Ile Ser Val Ile Thr Ile Phe Gly 65 70 75	238
CCT GTC AAC AAC AGC ACC ATG AAA ATC GAC CAC TTT CAG CTA GAT AAT Pro Val Asn Asn Ser Thr Met Lys Ile Asp His Phe Gln Leu Asp Asn 80 85 90 95	286
GAG AAG CCC ATG CGA GTG GTG GAT GAT GAA GAC TTG GTA GAC CAG CGT Glu Lys Pro Met Arg Val Val Asp Asp Glu Asp Leu Val Asp Gln Arg 100 105 110	334
CTC ATC AGC GAG CTG AGG AAA GAG TAC GGA ATG ACC TAC AAT GAC TTC Leu Ile Ser Glu Leu Arg Lys Glu Tyr Gly Met Thr Tyr Asn Asp Phe 115 120 125	382
TTC ATG GTG CTA ACA GAT GTG GAT CTG AGA GTC AAG CAA TAC TAT GAG Phe Met Val Leu Thr Asp Val Asp Leu Arg Val Lys Gln Tyr Tyr Glu 130 135 140	430
GTA CCA ATA ACA ATG AAG TCT GTG TTT GAT CTG ATC GAT ACT TTC CAG Val Pro Ile Thr Met Lys Ser Val Phe Asp Leu Ile Asp Thr Phe Gln 145 150 155	478
TCC CGA ATC AAA GAT ATG GAG AAG CAG AAG AAG GAG GGC ATT GTT TGC Ser Arg Ile Lys Asp Met Glu Lys Gln Lys Lys Glu Gly Ile Val Cys 160 165 170 175	526
AAA GAG GAA GTT GGG GGA GTG TTA GAA CTG TTC CCA ATT AAT GGG AGC Lys Glu Glu Val Gly Val Leu Glu Leu Phe Pro Ile Asn Gly Ser 180 185 190	574
TCT GTT GAG CGA GAA GAC GTC CCA GCC CAT TTG GTG AAA GAC ATT Ser Val Val Glu Arg Glu Asp Val Pro Ala His Leu Val Lys Asp Ile 195 200 205	622
CGT AAC TAT TTT CAA GTG AGC CCG GAG TAC TTC TCC ATG CTT CTA GTC Arg Asn Tyr Phe Gln Val Ser Pro Glu Tyr Phe Ser Met Leu Leu Val 210 215 220	670
GGA AAA GAC GGA AAT GTC AAA TCC TGG TAT CCT TCC CCA ATG TGG TCC Gly Lys Asp Gly Asn Val Lys Ser Trp Tyr Pro Ser Pro Met Trp Ser 225 230 235	718

ATG GTG ATT GTG TAC GAT TTA ATT GAT TCG ATG CAA CTT CGG AGA CAG Met Val Ile Val Tyr Asp Leu Ile Asp Ser Met Gln Leu Arg Arg Gln 240 245 250 255	766
GAA ATG GCG ATT CAG CAG TCA CTG GGG ATG CGC TGC CAG AAG ATG AGT Glu Met Ala Ile Gln Gln Ser Leu Gly Met Arg Cys Gln Lys Met Ser 260 265 270	814
ATG CAG GCT ATG GTT ACC ATA GTT ACC ACC AAG GAT ACC AGG ATG GTT Met Gln Ala Met Val Thr Ile Val Thr Thr Lys Asp Thr Arg Met Val 275 280 285	862
ACC AGG ATG ACT ACC GTC ATC ATG AGA GTT ATC ACC ACC ATG GAT ACC CTT Thr Arg Met Thr Thr Val Ile Met Arg Val Ile Thr Met Asp Thr Leu 290 295 300	910
ACT GAG CAG AAA TAT GTA ACC TTA GAC TCA GCC AGT TTC CTC TGC AGC Thr Glu Gln Lys Tyr Val Thr Leu Asp Ser Ala Ser Phe Leu Cys Ser 305 310 315	958
TGC TAAAACTACA TGTGGCCAGC TCCATTCTTC CACACTGCGT ACTACATTTC Cys 320	1011
CTGCCTTTT CTTTCAGTGT TTTTCTAAGA CTAATAAAT AGCAAACCTT CACCTAAAAA AAAAAAAAA AAAAAAA	1071
	1088

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 320 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Lys Lys Gly Gly Lys Thr Glu Gln Asp Gly Tyr Gln Lys Pro Thr Asn 1 5 10 15	
Lys His Phe Thr Gln Ser Pro Lys Lys Ser Val Ala Asp Leu Leu Gly 20 25 30	
Ser Phe Glu Gly Lys Arg Arg Leu Leu Ile Thr Ala Pro Lys Ala 35 40 45	
Glu Asn Asn Met Tyr Val Gln Gln Arg Asp Glu Tyr Leu Glu Ser Phe 50 55 60	
Cys Lys Met Ala Thr Arg Lys Ile Ser Val Ile Thr Ile Phe Gly Pro 65 70 75 80	
Val Asn Asn Ser Thr Met Lys Ile Asp His Phe Gln Leu Asp Asn Glu 85 90 95	
Lys Pro Met Arg Val Val Asp Asp Glu Asp Leu Val Asp Gln Arg Leu 100 105 110	
Ile Ser Glu Leu Arg Lys Glu Tyr Gly Met Thr Tyr Asn Asp Phe Phe 115 120 125	
Met Val Leu Thr Asp Val Asp Leu Arg Val Lys Gln Tyr Tyr Glu Val 130 135 140	

DEPARTMENT OF
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AND
MOLECULAR
BIOLOGY

Pro Ile Thr Met Lys Ser Val Phe Asp Leu Ile Asp Thr Phe Gln Ser
 145 150 155 160

Arg Ile Lys Asp Met Glu Lys Gln Lys Lys Glu Gly Ile Val Cys Lys
 165 170 175

Glu Glu Val Gly Gly Val Leu Glu Leu Phe Pro Ile Asn Gly Ser Ser
 180 185 190

Val Val Glu Arg Glu Asp Val Pro Ala His Leu Val Lys Asp Ile Arg
 195 200 205

Asn Tyr Phe Gln Val Ser Pro Glu Tyr Phe Ser Met Leu Leu Val Gly
 210 215 220

Lys Asp Gly Asn Val Lys Ser Trp Tyr Pro Ser Pro Met Trp Ser Met
 225 230 235 240

Val Ile Val Tyr Asp Leu Ile Asp Ser Met Gln Leu Arg Arg Gin Glu
 245 250 255

Met Ala Ile Gln Gln Ser Leu Gly Met Arg Cys Gln Lys Met Ser Met
 260 265 270

Gln Ala Met Val Thr Ile Val Thr Thr Lys Asp Thr Arg Met Val Thr
 275 280 285

Arg Met Thr Thr Val Ile Met Arg Val Ile Thr Met Asp Thr Leu Thr
 290 295 300

Glu Gln Lys Tyr Val Thr Leu Asp Ser Ala Ser Phe Leu Cys Ser Cys
 305 310 315 320

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1759 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..754

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

C AAA AAC TTC TTC CTG ACG AAT CGC GCC AGG GAG CGC TCA GAC ACC 46
 Lys Asn Phe Phe Leu Thr Asn Arg Ala Arg Glu Arg Ser Asp Thr
 1 5 10 15

TTC ATC AAC CTC CCG GAG GTG CTC AAC CGC TTC AAG CTG CCG CCA GGA 94
 Phe Ile Asn Leu Arg Glu Val Leu Asn Arg Phe Lys Leu Pro Pro Gly
 20 25 30

GAG TAC ATT CTC GTG CCT TCC ACC TTC GAA CCC AAC AAG GAT GGG GAT 142
 Glu Tyr Ile Leu Val Pro Ser Thr Phe Glu Pro Asn Lys Asp Gly Asp
 35 40 45

TTC TGC ATC CGG GTC TTT TCT GAA AAG AAA GCT GAC TAC CAA GCT GTC	190
Phe Cys Ile Arg Val Phe Ser Glu Lys Lys Ala Asp Tyr Gln Ala Val	
50 55 60	
GAT GAT GAA ATC GAG GCC AAT CTT GAA GAG TTC GAC ATC AGC GAG GAT	238
Asp Asp Glu Ile Glu Ala Asn Leu Glu Phe Asp Ile Ser Glu Asp	
65 70 75	
GAC ATT GAT GAT GGA TTC AGG AGA CTG TTT GCC CAG TTG GCA GGA GAG	286
Asp Ile Asp Asp Gly Phe Arg Arg Leu Phe Ala Gln Leu Ala Gly Glu	
80 85 90 95	
GAT GCG GAG ATC TCT GCC TTT GAG CTG CAG ACC ATC CTG AGA AGG GTT	334
Asp Ala Glu Ile Ser Ala Phe Glu Leu Gln Thr Ile Leu Arg Arg Val	
100 105 110	
CTA GCA AAG CGC CAA GAT ATC AAG TCA GAT GGC TTC AGC ATC GAG ACA	382
Leu Ala Lys Arg Gln Asp Ile Lys Ser Asp Gly Phe Ser Ile Glu Thr	
115 120 125	
TGC AAA ATT ATG GTT GAC ATG CTA GAT TCG GAC GGG AGT GGC AAG CTG	430
Cys Lys Ile Met Val Asp Met Leu Asp Ser Asp Gly Ser Gly Lys Leu	
130 135 140	
GGG CTG AAG GAG TTC TAC ATT CTC TGG ACG AAG ATT CAA AAA TAC CAA	478
Gly Leu Lys Glu Phe Tyr Ile Leu Trp Thr Lys Ile Gln Lys Tyr Gln	
145 150 155	
AAA ATT TAC CGA GAA ATC GAC GTT GAC AGG TCT GGT ACC ATG AAT TCC	526
Lys Ile Tyr Arg Glu Ile Asp Val Asp Arg Ser Gly Thr Met Asn Ser	
160 165 170 175	
TAT GAA ATG CGG AAG GCA TTA GAA GAA GCA GGT TTC AAG ATG CCC TGT	574
Tyr Glu Met Arg Lys Ala Leu Glu Ala Gly Phe Lys Met Pro Cys	
180 185 190	
CAA CTC CAC CAA GTC ATC GTT GCT CGG TTT GCA GAT GAC CAG CTC ATC	622
Gln Leu His Gln Val Ile Val Ala Arg Phe Ala Asp Asp Gln Leu Ile	
195 200 205	
ATC GAT TTT GAT AAT TTT GTT CCG TGT TTG GTT CCG CTG GAA ACG CTA	670
Ile Asp Phe Asp Asn Phe Val Arg Cys Leu Val Arg Leu Glu Thr Leu	
210 215 220	
TTC AAG ATA TTT AAG CAG CTG GAT CCC GAG AAT ACT GGA ACA ATA GAG	718
Phe Lys Ile Phe Lys Gln Leu Asp Pro Glu Asn Thr Gly Thr Ile Glu	
225 230 235	
CTC GAC CTT ATC TCT TGG CTC TGT TTC TCA GTA CTT TGAAGTTATA	764
Leu Asp Leu Ile Ser Trp Leu Cys Phe Ser Val Leu	
240 245 250	
ACTAACCTGC CTGAAGACTT CTCATGATGG AAAATCAGCC AAGGACTAAG CTTCCATAGA	824
AATAACACTTT GTATCTGGAC CTCAAAATTAA TGGAACATT TACTTAAACG GATGATCATA	884
GCTGAAAATA ATGATACTGT CAATTTGAGA TAGCAGAAAGT TTCACACATC AAAGTAAAAG	944
ATTTGCATAT CATTATACTA AATGCAAATG AGTCGCTTAA CCCTTGACAA GGTCAAAGAG	1004
AGCTTTAAAT CTGTAAATAG TATACACTTT TTACTTTAC ACACCTTCCT GTTCATAGCA	1064
ATATTAAATC AGGAAAAAAA AATGCAGGGA GGTATTTAAC AGCTGAGCAA AACACATTGAG	1124
TCGCTCTCAA AGGACACGAG GCCCTTGGCA GGGATATTAAAGCAACTTGAGCTTTAA	1184
ATGCAGCTGT TGATTCTACC AAACAACAGT CCAAGATTAC CATTCCCAC GAGCCAATG	1244

GGAAACATGG TATATCATGA AGTAATCTTG TCAAGGCATC TGGAGAGTCC AGGAGAGAAG	1304
ACTCACCTCT GTCGCTTGGG TTAAACAAGA GACAGGTTTT GTAGAATATT GATTGGTAAT	1364
AGTAAATCGT TCTCCTTACA ATCAAGTTCT TGACCCTATT CGGCCTTATA CATCTGGTCT	1424
TACAAAAGACC AAAGGGATCC TGCCTTGAT CAACTGAACC AGTATGCCAA AACCAAGGCAT	1484
CCAATTGTA AACCAATTAT GATAAAGGAC AAAATAAGCT GTTGCCACC TCAAAACTTT	1544
ATGAACTTCA CCACCACTAG TGTCTGTCCA TGGAGTTAGA GGGGACATCA CTTAGAAGTT	1604
CTTATAGAAA GGACACAAAGT TTGTTTCCTG GCTTACCTT GGGAAATGC TAGAACATT	1664
ATAGAAATTT TGCCTTGTG CCTTATCTTC TTCCAAATGT ACTGTTAAAT AAAAATAAAG	1724
GGTTACCCCCA TGCAATCAAA AAAAAAAA AAAAA	1759

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 251 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Lys Asn Phe Phe Leu Thr Asn Arg Ala Arg Glu Arg Ser Asp Thr Phe			
1	5	10	15
Ile Asn Leu Arg Glu Val Leu Asn Arg Phe Lys Leu Pro Pro Gly Glu			
20	25	30	
Tyr Ile Leu Val Pro Ser Thr Phe Glu Pro Asn Lys Asp Gly Asp Phe			
35	40	45	
Cys Ile Arg Val Phe Ser Glu Lys Lys Ala Asp Tyr Gln Ala Val Asp			
50	55	60	
Asp Glu Ile Glu Ala Asn Leu Glu Glu Phe Asp Ile Ser Glu Asp Asp			
65	70	75	80
Ile Asp Asp Gly Phe Arg Arg Leu Phe Ala Gln Leu Ala Gly Glu Asp			
85	90	95	
Ala Glu Ile Ser Ala Phe Glu Leu Gln Thr Ile Leu Arg Arg Val Leu			
100	105	110	
Ala Lys Arg Gln Asp Ile Lys Ser Asp Gly Phe Ser Ile Glu Thr Cys			
115	120	125	
Lys Ile Met Val Asp Met Leu Asp Ser Asp Gly Ser Gly Lys Leu Gly			
130	135	140	
Leu Lys Glu Phe Tyr Ile Leu Trp Thr Lys Ile Gln Lys Tyr Gln Lys			
145	150	155	160
Ile Tyr Arg Glu Ile Asp Val Asp Arg Ser Gly Thr Met Asn Ser Tyr			
165	170	175	
Glu Met Arg Lys Ala Leu Glu Glu Ala Gly Phe Lys Met Pro Cys Gln			
180	185	190	

Leu His Gln Val Ile Val Ala Arg Phe Ala Asp Asp Gln Leu Ile Ile
195 200 205

Asp Phe Asp Asn Phe Val Arg Cys Leu Val Arg Leu Glu Thr Leu Phe
210 215 220

Lys Ile Phe Lys Gln Leu Asp Pro Glu Asn Thr Gly Thr Ile Glu Leu
225 230 235 240

Asp Leu Ile Ser Trp Leu Cys Phe Ser Val Leu
245 250

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 700 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Ala Gly Ile Ala Ala Lys Leu Ala Lys Asp Arg Glu Ala Ala Glu
1 5 10 15

Gly Leu Gly Ser His Glu Arg Ala Ile Lys Tyr Leu Asn Gln Asp Tyr
20 25 30

Glu Ala Leu Arg Asn Glu Cys Leu Glu Ala Gly Thr Leu Phe Gln Asp
35 40 45

Pro Ser Phe Pro Ala Ile Pro Ser Ala Leu Gly Phe Lys Glu Leu Gly
50 55 60

Pro Tyr Ser Ser Lys Thr Arg Gly Met Arg Trp Lys Arg Pro Thr Glu
65 70 75 80

Ile Cys Ala Asp Pro Gln Phe Ile Ile Gly Gly Ala Thr Arg Thr Asp
85 90 95

Ile Cys Gln Gly Ala Leu Gly Asp Cys Trp Leu Leu Ala Ala Ile Ala
100 105 110

Ser Leu Thr Leu Asn Glu Glu Ile Leu Ala Arg Val Val Pro Leu Asn
115 120 125

Gln Ser Phe Gln Glu Asn Tyr Ala Gly Ile Phe His Phe Gln Phe Trp
130 135 140

Gln Tyr Gly Glu Trp Val Glu Val Val Val Asp Asp Arg Leu Pro Thr
145 150 155 160

Lys Asp Gly Glu Leu Leu Phe Val His Ser Ala Glu Gly Ser Glu Phe
165 170 175

Trp Ser Ala Leu Leu Glu Lys Ala Tyr Ala Lys Ile Asn Gln Cys Tyr
180 185 190

Glu Ala Leu Ser Gly Gly Ala Thr Thr Glu Gly Phe Glu Asp Phe Thr
195 200 205

Gly Gly Ile Ala Glu Trp Tyr Glu Leu Lys Lys Pro Pro Pro Asn Leu
210 215 220

Phe Lys Ile Ile Gln Lys Ala Leu Gln Lys Gly Ser Leu Leu Gly Cys
225 230 235 240

Ser Ile Asp Ile Thr Ser Ala Ala Asp Ser Glu Ala Ile Thr Phe Gln
245 250 255

Lys Leu Val Lys Gly His Ala Tyr Ser Val Thr Gly Ala Glu Glu Val
260 265 270

Glu Ser Asn Gly Ser Leu Gln Lys Leu Ile Arg Ile Arg Asn Pro Trp
275 280 285

Gly Glu Val Glu Trp Thr Gly Arg Trp Asn Asp Asn Cys Pro Ser Trp
290 295 300

Asn Thr Ile Asp Pro Glu Glu Arg Glu Arg Leu Thr Arg Arg His Glu
305 310 315 320

Asp Gly Glu Phe Trp Met Ser Phe Ser Asp Phe Leu Arg His Tyr Ser
325 330 335

Arg Leu Glu Ile Cys Asn Leu Thr Pro Asp Thr Leu Thr Ser Asp Thr
340 345 350

Tyr Lys Lys Trp Lys Leu Thr Lys Met Asp Gly Asn Trp Arg Arg Gly
355 360 365

Ser Thr Ala Gly Gly Cys Arg Asn Tyr Pro Asn Thr Phe Trp Met Asn
370 375 380

Pro Gln Tyr Leu Ile Lys Leu Glu Glu Glu Asp Glu Asp Glu Asp
385 390 395 400

Gly Glu Ser Gly Cys Thr Phe Leu Val Gly Leu Ile Gln Lys His Arg
405 410 415

Arg Arg Gln Arg Lys Met Gly Glu Asp Met His Thr Ile Gly Phe Gly
420 425 430

Ile Tyr Glu Val Pro Glu Glu Leu Ser Gly Gln Thr Asn Ile His Leu
435 440 445

Ser Lys Asn Phe Phe Leu Thr Asn Arg Ala Arg Glu Arg Ser Asp Thr
450 455 460

Phe Ile Asn Leu Arg Glu Val Leu Asn Arg Phe Lys Leu Pro Pro Gly
465 470 475 480

Glu Tyr Ile Leu Val Pro Ser Thr Phe Glu Pro Asn Lys Asp Gly Asp
485 490 495

Phe Cys Ile Arg Val Phe Ser Glu Lys Lys Ala Asp Tyr Gln Ala Val
500 505 510

Asp Asp Glu Ile Glu Ala Asn Leu Glu Glu Phe Asp Ile Ser Glu Asp
515 520 525

Asp Ile Asp Asp Gly Val Arg Arg Leu Phe Ala Gln Leu Ala Gly Glu
530 535 540

Asp Ala Glu Ile Ser Ala Phe Glu Leu Gln Thr Ile Leu Arg Arg Val
545 550 555 560

Leu Ala Lys Arg Gln Asp Ile Lys Ser Asp Gly Phe Ser Ile Glu Thr
565 570 575

Cys Lys Ile Met Val Asp Met Leu Asp Ser Asp Gly Ser Gly Lys Leu
580 585 590

Gly Leu Lys Glu Phe Tyr Ile Leu Trp Thr Lys Ile Gln Lys Tyr Gln
595 600 605

Lys Ile Tyr Arg Glu Ile Asp Val Asp Arg Ser Gly Thr Met Asn Ser
610 615 620

Tyr Glu Met Arg Lys Ala Leu Glu Glu Ala Gly Phe Lys Met Pro Cys
625 630 635 640

Gln Leu His Gln Val Ile Val Ala Arg Phe Ala Asp Asp Gln Leu Ile
645 650 655

Ile Asp Phe Asp Asn Phe Val Arg Cys Leu Val Arg Leu Glu Thr Leu
660 665 670

Phe Lys Ile Phe Lys Gln Leu Asp Pro Glu Asn Thr Gly Thr Ile Glu
675 680 685

Leu Asp Leu Ile Ser Trp Leu Cys Phe Ser Val Leu
690 695 700